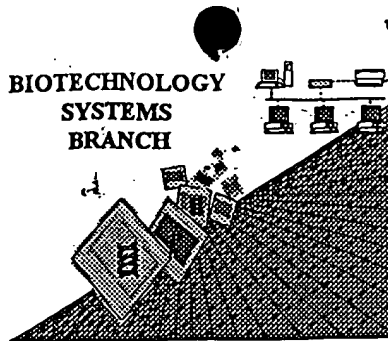


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

APR 11 2002

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/995,587
Source: OIP
Date Processed by STIC: 12/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

APR 11 2002

Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER:

TECH/001/SPR 600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

APR 11 2002

TECH CENTER 1600/2900

OIPE

RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/995,587

TIME: 11:29:22

Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I995587.raw

3 <110> APPLICANT: TNO
5 <120> TITLE OF INVENTION: Novel fructosyltransferases
7 <130> FILE REFERENCE: Novel fructosyltransferases
9 <140> CURRENT APPLICATION NUMBER: US/09/995,587
10 <141> CURRENT FILING DATE: 2001-11-29
12 <150> PRIOR APPLICATION NUMBER: 00201872.9
13 <151> PRIOR FILING DATE: 2000-05-25
15 <150> PRIOR APPLICATION NUMBER: 01200049.3
16 <151> PRIOR FILING DATE: 2001-01-09
18 <160> NUMBER OF SEQ ID NOS: 26
20 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

pp 1-4

ERRORED SEQUENCES

401 <210> SEQ ID NO: 5
402 <211> LENGTH: 5
403 <212> TYPE: PRT
404 <213> ORGANISM: Lactobacillus reuteri
406 <400> SEQUENCE: 5
E--> 407 Leu Pro Xaa Thr Gly *see item 9 on Error Summary Sheet*
408 1 5
753 <210> SEQ ID NO: 11
754 <211> LENGTH: 792
755 <212> TYPE: PRT
756 <213> ORGANISM: Lactobacillus reuteri
758 <400> SEQUENCE: 11
759 Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala Thr Leu Val Ser Ala
760 1 5 10 15
762 Ser Ile Leu Met Gly Gly Val Val Thr Ala His Ala Asp Gln Val Glu
763 20 25 30
765 Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala
766 35 40 45
768 Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn
769 50 55 60
771 Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser Ala Thr Asn Asn Thr
772 65 70 75 80
774 Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn
775 85 90 95
777 Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Ala Val
778 100 105 110
780 Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Asp Asn Ser Gln
781 115 120 125
783 Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala Ala Thr Gln Ala Asn
784 130 135 140
786 Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala Val Gln Asn Ala Lys
787 145 150 155 160

pp 2-3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/995,587

DATE: 12/06/2001

TIME: 11:29:22

Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I995587.raw

```

789 Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile Asn Glu Leu Asn Lys
790      165      170      175
792 Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala Lys Leu Thr Phe Lys
793      180      185      190
795 Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys Gln Asp Pro Gln Tyr
796      195      200      205
798 Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys Asn Met Pro Ala Thr
799      210      215      220
801 Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala His Leu Asp Val Trp
802 225      230      235      240
804 Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly Tyr Val Ser Asn Tyr
805      245      250      255
807 Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly Ile Pro Asn Ser Pro
808      260      265      270
810 Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys Tyr Gly Asp Asn
811      275      280      285
813 Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile Phe Gly Thr Lys Glu
814      290      295      300
816 Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala Ile Val Asn Asp Asp
817 305      310      315      320
819 Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp Thr Ser Asp Tyr Lys
820      325      330      335
822 Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu Asn Leu Asn Val Asp
823      340      345      350
825 Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn Tyr Gln Val Leu Phe
826      355      360      365
828 Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu Gln Phe Ala Asn Gly
829      370      375      380
831 Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg Asp Pro His Val Val
832 385      390      395      400
834 Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala Asn Thr Gly
835      405      410      415
837 Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr Asn Trp Ala Asn Tyr
838      420      425      430
840 Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser Phe Lys Leu Leu Asn
841      435      440      445
843 Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala Asn Gly Ala Leu Gly
844      450      455      460
846 Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro Lys Val Glu Glu Val
847 465      470      475      480
E--> 849 Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys Asp Glu Val Xaa Xaa
850      485      490      495
852 Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val Thr Arg Val Ser Arg
853      500      505      510
855 Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn Thr Ile Val Gly Asp
856      515      520      525
858 Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser Leu Met Gly Lys Tyr
859      530      535      540
861 Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr Ala Ser Val Pro Ala

```

see item 9

DATE: 12/06/2001

TIME: 11:29:22

Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I995587.raw

	862	545				550				555					560	
	864	Asn	Trp	Arg	Thr	Ala	Thr	Tyr	Ser	Tyr	Tyr	Ala	Val	Pro	Val	Ala
	865					565					570				575	
	867	His	Pro	Asp	Gln	Val	Leu	Ile	Thr	Ser	Tyr	Met	Ser	Asn	Lys	Asp
	868					580					585				590	
	870	Ala	Ser	Gly	Glu	Gly	Asn	Tyr	Ala	Thr	Trp	Ala	Pro	Ser	Phe	Leu
	871					595				600				605		
	873	Gln	Ile	Asn	Pro	Asp	Asp	Thr	Thr	Thr	Val	Leu	Ala	Arg	Ala	Thr
	874		610						615				620			
	876	Gln	Gly	Asp	Trp	Val	Trp	Asp	Asp	Ser	Ser	Arg	Asn	Asp	Asn	Met
	877	625					630					635				
	879	Gly	Val	Leu	Lys	Glu	Gly	Ala	Ala	Asn	Ser	Ala	Ala	Leu	Pro	Gly
	880					645					650				655	
	882	Trp	Gly	Lys	Pro	Val	Asp	Trp	Ser	Leu	Ile	Asn	Arg	Ser	Pro	Gly
	883				660					665					670	
	885	Gly	Leu	Lys	Pro	His	Gln	Pro	Val	Gln	Pro	Lys	Ile	Asp	Gln	Pro
	886			675					680					685		
	888	Gln	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn
	889		690					695					700			
	891	Asp	Lys	Pro	Ala	Gly	Lys	Ala	Thr	Pro	Asp	Asn	Thr	Asn	Ile	Asp
	892	705					710					715				
	894	Ser	Ala	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Asn	Ile	Asp	Pro	Ser	Ala
	895					725					730				735	
E-->	897	Xaa	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn	Glu	Lys
	898				740					745				750		
	900	Gly	Lys	Asn	Thr	Asp	Ala	Lys	Gln	Leu	Pro	Gln	Thr	Gly	Asn	Lys
	901			755					760					765		
	903	Gly	Leu	Ala	Gly	Leu	Tyr	Ala	Gly	Ser	Leu	Leu	Ala	Leu	Phe	Gly
	904		770					775					780			
	906	Ala	Ala	Ile	Glu	Lys	Arg	His	Ala							
	907	785						790								

1079 <210> SEQ ID NO: 26

1080 <211> LENGTH: 21

1081 <212> TYPE: DNA

1082 <213> ORGANISM:

1082 <213> ORGANISM: Artificial Sequence

1084 <220> FEATURE:

1085 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

1087 <400> .SEQUENCE: 26

W--> 1088 tacconwsnc tacttcaact t

21

E--> 1093

delete
at end
of file.

see next page

gat gag gta (nnn nnn) aag ctt ggt gat aag tat tat ctc ttc tcc gta 2740
 Asp Glu Val Xaa Xaa Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val
 495 500 505

(portion of Sequence 10)

more n's are shown in Sequence 10-

the above n's are shown as a
sample of error

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/995,587

DATE: 12/06/2001

TIME: 11:29:24

Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I995587.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
 L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:407 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
 L:640 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:641 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:701 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:718 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:849 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
 M:340 Repeated in SeqNo=11
 L:992 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
 L:992 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
 L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1004 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
 L:1004 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
 L:1004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:1040 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
 L:1040 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
 L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 L:1052 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
 L:1052 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
 L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:1088 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
 L:1088 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
 L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
 L:1093 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:21 SEQ:26